IN THE CLAIMS:

Please amend the claims and add new claims as follows:

18. (Amended) A method of predicting therapeutic efficacy of treatment of a multiple sclerosis patient with a peptide of from ~~about 8 to about 25~~ 7 to 46 amino acids and having a sequence contained within amino acid residues 61-106 of SEQ ID NO:1, including substitutions, additions or deletions thereof, provided the peptide is capable of neutralizing or modulating the production of anti-myelin basic protein, comprising screening a multiple sclerosis patient for the presence of an human leukocyte antigen (HLA)-DR2 ~~HLA-DR2~~ haplotype, wherein the presence of the human leukocyte antigen (HLA)-DR2 ~~HLA-DR2~~ haplotype in the patient is predictive of therapeutic efficacy of treatment with the peptide.

19. (Amended) The method of ~~any of claims 1 to 3~~ claim 18, wherein the human leukocyte antigen (HLA)-DR2 ~~HLA-DR2~~ haplotype comprises DRB1*1501 or DRB1*15021.

20. (Amended) The method of ~~any of claims 1 to 3~~ claim 18, wherein the patient has chronic progressive multiple sclerosis (MS) ~~MS~~.

21. (New) A method of predicting therapeutic efficacy of treatment of a multiple sclerosis patient with a peptide of from 7 to 46 amino acids and having a sequence contained within amino acid residues 61-106 of SEQ ID NO:1, comprising screening a multiple sclerosis patient for the presence of an human leukocyte antigen (HLA)-DR2 haplotype, wherein the presence of the human leukocyte antigen (HLA)-DR2 haplotype in the patient is predictive of therapeutic efficacy of treatment with the peptide.

22. (New) A method of predicting therapeutic efficacy of treatment of a multiple sclerosis patient with a peptide of from 8 to 25 amino acids and having a sequence contained within amino acid residues 61-106 of SEQ ID NO:1, including substitutions, additions or

deletions thereof, provided the peptide is capable of neutralizing or modulating the production of anti-myelin basic protein, comprising screening a multiple sclerosis patient for the presence of an human leukocyte antigen (HLA)-DR2 haplotype, wherein the presence of the human leukocyte antigen (HLA)-DR2 haplotype in the patient is predictive of therapeutic efficacy of treatment with the peptide.

23. (New) A method of predicting therapeutic efficacy of treatment of a multiple sclerosis patient with a peptide of from 8 to 25 amino acids and having a sequence contained within amino acid residues 61-106 of SEQ ID NO:1, comprising screening a multiple sclerosis patient for the presence of an human leukocyte antigen (HLA)-DR2 haplotype, wherein the presence of the human leukocyte antigen (HLA)-DR2 haplotype in the patient is predictive of therapeutic efficacy of treatment with the peptide.

24. (New) A method of predicting therapeutic efficacy of treatment of a multiple sclerosis patient with a peptide having a sequence with the formula: R_1-Val-His-Phe-Phe-Lys-Asn-Ile-R_2 (SEQ ID NO:2) and salts thereof, wherein R_1 and R_2 are independently selected from the group consisting of hydrogen, hydroxy, the residue of an amino acid and the residue of a polypeptide; provided that R_1 and R_2 are not both hydrogen or hydroxyl at the same time, comprising screening a multiple sclerosis patient for the presence of an human leukocyte antigen (HLA)-DR2 haplotype, wherein the presence of the human leukocyte antigen (HLA)-DR2 haplotype in the patient is predictive of therapeutic efficacy of treatment with the peptide.

25. (New) The method of claim 24, wherein R_1 or R_2 is a naturally occurring amino acid.